

R. Prouty

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1652

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/697,898

DATE: 12/05/2001

TIME: 10:21:14

Input Set : A:\103576-144.ST25.txt

Output Set: N:\CRF3\12052001\I697898.raw

3 <110> APPLICANT: Palombella, Vito J.  
4 Liao, Sha-Mei  
6 <120> TITLE OF INVENTION: MEKK1 Molecules and Uses Thereof  
8 <130> FILE REFERENCE: 103576.144  
10 <140> CURRENT APPLICATION NUMBER: US 09/697,898  
11 <141> CURRENT FILING DATE: 2000-10-27  
13 <160> NUMBER OF SEQ ID NOS: 28  
15 <170> SOFTWARE: PatentIn version 3.0  
17 <210> SEQ ID NO: 1  
18 <211> LENGTH: 5245  
19 <212> TYPE: DNA  
20 <213> ORGANISM: Human  
22 <220> FEATURE:  
23 <221> NAME/KEY: CDS  
24 <222> LOCATION: (7)..(4545)  
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29 1 5 10  
31 ccg ggc gcc agg gct acg agc cct gag gca ggc ggc ggc gga gga gcc 96  
32 Pro Gly Ala Arg Ala Thr Ser Pro Glu Ala Gly Gly Gly Gly Ala  
33 15 20 25 30  
35 ctc aag gcg agc agc gcg ccc gcg gct gcc gcg gga ctg ctg cgg gag 144  
36 Leu Lys Ala Ser Ser Ala Pro Ala Ala Ala Gly Leu Leu Arg Glu  
37 35 40 45  
39 gcg ggc agc ggg ggc cgc gag cgg gcg gac tgg cgg cgg cgg cag ctg 192  
40 Ala Gly Ser Gly Gly Arg Glu Arg Ala Asp Trp Arg Arg Arg Gln Leu  
41 50 55 60  
43 cgc aaa gtg cgg agt gtg gag ctg gac cag ctg cct gag cag ccg ctc 240  
44 Arg Lys Val Arg Ser Val Glu Leu Asp Gln Leu Pro Glu Gln Pro Leu  
45 65 70 75  
47 ttc ctt gcc gcc tca ccg ccg gcc tcc tcg act tcc ccg tcg ccg gag 288  
48 Phe Leu Ala Ala Ser Pro Pro Ala Ser Ser Thr Ser Pro Ser Pro Glu  
49 80 85 90  
51 ccc gcg gac gca gcg ggg agt ggg acc ggc ttc cag cct gtg gcg gtg 336  
52 Pro Ala Asp Ala Ala Gly Ser Gly Thr Gly Phe Gln Pro Val Ala Val  
53 95 100 105 110  
55 ccg ccg ccc cac gga gcc gcg agc cgc ggc ggc gcc cac ctt acc gag 384  
56 Pro Pro Pro His Gly Ala Ala Ser Arg Gly Gly Ala His Leu Thr Glu  
57 115 120 125  
59 tcg gtg gcg gcg ccg gac agc ggc gcc tcg agt ccc gca gcg gcc gag 432  
60 Ser Val Ala Ala Pro Asp Ser Gly Ala Ser Ser Pro Ala Ala Glu  
61 130 135 140  
63 ccc ggg gag aag cgg gcg ccc gcc gcc gag ccg tct cct gca gcg gcc 480  
64 Pro Gly Glu Lys Arg Ala Pro Ala Ala Glu Pro Ser Pro Ala Ala Ala  
65 145 150 155  
67 ccc gcc ggt cgt gag atg gag aat aaa gaa act ctc aaa ggg ttg cac 528

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69      160                      165                      170
71 aag atg gat gat cgt cca gag gaa cga atg atc agg gag aaa ctg aag      576
72 Lys Met Asp Asp Arg Pro Glu Glu Arg Met Ile Arg Glu Lys Leu Lys
73 175                      180                      185                      190
75 gca acc tgt atg cca gcc tgg aag cac gaa tgg ttg gaa agg aga aat      624
76 Ala Thr Cys Met Pro Ala Trp Lys His Glu Trp Leu Glu Arg Arg Asn
77      195                      200                      205
79 agg cga ggg cct gtg gtg gta aaa cca atc cca gtt aaa gga gat gga      672
80 Arg Arg Gly Pro Val Val Val Lys Pro Ile Pro Val Lys Gly Asp Gly
81      210                      215                      220
83 tct gaa atg aat cac tta gca gct gag tct cca gga gag gtc cag gca      720
84 Ser Glu Met Asn His Leu Ala Ala Glu Ser Pro Gly Glu Val Gln Ala
85      225                      230                      235
87 agt gcg gct tca cca gct tcc aaa ggc cga cgc agt cct tct cct ggc      768
88 Ser Ala Ala Ser Pro Ala Ser Lys Gly Arg Arg Ser Pro Ser Pro Gly
89      240                      245                      250
91 aac tcc cca tca ggt cgc aca gtg aaa tca gaa tct cca gga gta agg      816
92 Asn Ser Pro Ser Gly Arg Thr Val Lys Ser Glu Ser Pro Gly Val Arg
93 255                      260                      265                      270
95 aga aaa aga gtt tcc cca gtg cct ttt cag agt ggc aga atc aca cca      864
96 Arg Lys Arg Val Ser Pro Val Pro Phe Gln Ser Gly Arg Ile Thr Pro
97      275                      280                      285
99 ccc cga aga gcc cct tca cca gat ggc ttc tca cca tat agc cct gag      912
100 Pro Arg Arg Ala Pro Ser Pro Asp Gly Phe Ser Pro Tyr Ser Pro Glu
101      290                      295                      300
103 gaa aca aac cgc cgt gtt aac aaa gtg atg cgg gcc aga ctg tac tta      960
104 Glu Thr Asn Arg Arg Val Asn Lys Val Met Arg Ala Arg Leu Tyr Leu
105      305                      310                      315
107 ctg cag cag ata ggg cct aac tct ttc ctg att gga gga gac agc cca      1008
108 Leu Gln Gln Ile Gly Pro Asn Ser Phe Leu Ile Gly Gly Asp Ser Pro
109      320                      325                      330
111 gac aat aaa tac cgg gtg ttt att ggg cct cag aac tgc agc tgt gca      1056
112 Asp Asn Lys Tyr Arg Val Phe Ile Gly Pro Gln Asn Cys Ser Cys Ala
113 335                      340                      345                      350
115 cgt gga aca ttc tgt att cat ctg cta ttt gtg atg ctc cgg gtg ttt      1104
116 Arg Gly Thr Phe Cys Ile His Leu Leu Phe Val Met Leu Arg Val Phe
117      355                      360                      365
119 caa cta gaa cct tca gac cca atg tta tgg aga aaa act tta aag aat      1152
120 Gln Leu Glu Pro Ser Asp Pro Met Leu Trp Arg Lys Thr Leu Lys Asn
121      370                      375                      380
123 ttt gag gtt gag agt ttg ttc cag aaa tat cac agt agg cgt agc tca      1200
124 Phe Glu Val Glu Ser Leu Phe Gln Lys Tyr His Ser Arg Arg Ser Ser
125      385                      390                      395
127 agg atc aaa gct cca tct cgt aac acc atc cag aag ttt gtt tca cgc      1248
128 Arg Ile Lys Ala Pro Ser Arg Asn Thr Ile Gln Lys Phe Val Ser Arg
129      400                      405                      410
131 atg tca aat tct cat aca ttg tca tca tct agt act tct acg tct agt      1296
132 Met Ser Asn Ser His Thr Leu Ser Ser Ser Ser Thr Ser Thr Ser Ser

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133	415		420		425		430	
135	tca gaa aac agc ata aag gat gaa gag gaa cag atg tgt cct att tgc						1344	
136	Ser Glu Asn Ser Ile Lys Asp Glu Glu Glu Gln Met Cys Pro Ile Cys							
137		435		440		445		
139	ttg ttg ggc atg ctt gat gaa gaa agt ctt aca gtg tgt gaa gac ggc						1392	
140	Leu Leu Gly Met Leu Asp Glu Glu Ser Leu Thr Val Cys Glu Asp Gly							
141		450		455		460		
143	tgc agg aac aag ctg cac cac cac tgc atg tca att tgg gca gaa gag						1440	
144	Cys Arg Asn Lys Leu His His His Cys Met Ser Ile Trp Ala Glu Glu							
145		465		470		475		
147	tgt aga aga aat aga gaa cct tta ata tgt ccc ctt tgt aga tct aag						1488	
148	Cys Arg Arg Asn Arg Glu Pro Leu Ile Cys Pro Leu Cys Arg Ser Lys							
149		480		485		490		
151	tgg aga tct cat gat ttc tac agc cac gag ttg tca agt cct gtg gat						1536	
152	Trp Arg Ser His Asp Phe Tyr Ser His Glu Leu Ser Ser Pro Val Asp							
153	495		500		505		510	
155	tcc cct tct tcc ctc aga gct gca cag cag caa acc gta cag cag cag						1584	
156	Ser Pro Ser Ser Leu Arg Ala Ala Gln Gln Gln Thr Val Gln Gln Gln							
157		515		520		525		
159	cct ttg gct gga tca cga agg aat caa gag agc aat ttt aac ctt act						1632	
160	Pro Leu Ala Gly Ser Arg Arg Asn Gln Glu Ser Asn Phe Asn Leu Thr							
161		530		535		540		
163	cat tat gga act cag caa atc cct cct gct tac aaa gat tta gct gag						1680	
164	His Tyr Gly Thr Gln Gln Ile Pro Pro Ala Tyr Lys Asp Leu Ala Glu							
165		545		550		555		
167	cca tgg att cag gtg ttt gga atg gaa ctc gtt ggc tgc tta ttt tct						1728	
168	Pro Trp Ile Gln Val Phe Gly Met Glu Leu Val Gly Cys Leu Phe Ser							
169		560		565		570		
171	aga aac tgg aat gtg aga gag atg gcc ctc agg cgt ctt tcc cat gat						1776	
172	Arg Asn Trp Asn Val Arg Glu Met Ala Leu Arg Arg Leu Ser His Asp							
173	575		580		585		590	
175	gtc agt ggg gcc ctg ctg ttg gca aat ggg gag agc act gga aat tct						1824	
176	Val Ser Gly Ala Leu Leu Ala Asn Gly Glu Ser Thr Gly Asn Ser							
177		595		600		605		
179	ggg ggc agc agt gga agc agc ccg agt ggg gga gcc acc agt ggg tct						1872	
180	Gly Gly Ser Ser Gly Ser Ser Pro Ser Gly Gly Ala Thr Ser Gly Ser							
181		610		615		620		
183	tcc cag acc agt atc tca gga gat gtg gtg gag gca tgc tgc agc gtt						1920	
184	Ser Gln Thr Ser Ile Ser Gly Asp Val Val Glu Ala Cys Cys Ser Val							
185		625		630		635		
187	ctg tca atg gtc tgt gct gac cct gtc tac aaa gtg tac gtt gct gct						1968	
188	Leu Ser Met Val Cys Ala Asp Pro Val Tyr Lys Val Tyr Val Ala Ala							
189		640		645		650		
191	tta aaa aca ttg aga gcc atg ctg gta tat act cct tgc cac agt tta						2016	
192	Leu Lys Thr Leu Arg Ala Met Leu Val Tyr Thr Pro Cys His Ser Leu							
193	655		660		665		670	
195	gcg gaa aga atc aaa ctt cag aga ctt ctc cag cca gtt gta gac acc						2064	
196	Ala Glu Arg Ile Lys Leu Gln Arg Leu Leu Gln Pro Val Val Asp Thr							
197		675		680		685		

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199	atc	cta	gtc	aaa	tgt	gca	gat	gcc	aat	agc	cgc	aca	agt	cag	ctg	tcc	2112
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201				690					695					700			
203	ata	tca	aca	ctg	ttg	gaa	ctg	tgc	aaa	ggc	caa	gca	gga	gag	ttg	gca	2160
204	Ile	Ser	Thr	Leu	Leu	Glu	Leu	Cys	Lys	Gly	Gln	Ala	Gly	Glu	Leu	Ala	
205				705				710						715			
207	gtt	ggc	aga	gaa	ata	cta	aaa	gct	gga	tcc	att	ggg	att	ggg	ggg	gtt	2208
208	Val	Gly	Arg	Glu	Ile	Leu	Lys	Ala	Gly	Ser	Ile	Gly	Ile	Gly	Gly	Val	
209				720				725						730			
211	gat	tat	gtc	tta	aat	tgt	att	ctt	gga	aac	caa	act	gaa	tca	aac	aat	2256
212	Asp	Tyr	Val	Leu	Asn	Cys	Ile	Leu	Gly	Asn	Gln	Thr	Glu	Ser	Asn	Asn	
213	735					740					745					750	
215	tgg	caa	gaa	ctt	ctt	ggc	cgc	ctt	tgt	ctt	ata	gat	aga	ctg	ttg	ttg	2304
216	Trp	Gln	Glu	Leu	Leu	Gly	Arg	Leu	Cys	Leu	Ile	Asp	Arg	Leu	Leu	Leu	
217				755					760						765		
219	gaa	ttt	cct	gct	gaa	ttt	tat	cct	cat	att	gtc	agt	act	gat	gtt	tca	2352
220	Glu	Phe	Pro	Ala	Glu	Phe	Tyr	Pro	His	Ile	Val	Ser	Thr	Asp	Val	Ser	
221				770					775					780			
223	caa	gct	gag	cct	gtt	gaa	atc	agg	tat	aag	aag	ctg	ctg	tcc	ctc	tta	2400
224	Gln	Ala	Glu	Pro	Val	Glu	Ile	Arg	Tyr	Lys	Lys	Leu	Leu	Ser	Leu	Leu	
225				785				790						795			
227	acc	ttt	gct	ttg	cag	tcc	att	gat	aat	tcc	cac	tca	atg	gtt	ggc	aaa	2448
228	Thr	Phe	Ala	Leu	Gln	Ser	Ile	Asp	Asn	Ser	His	Ser	Met	Val	Gly	Lys	
229				800				805					810				
231	ctt	tcc	aga	agg	atc	tac	ttg	agt	tct	gca	aga	atg	gtt	act	aca	gta	2496
232	Leu	Ser	Arg	Arg	Ile	Tyr	Leu	Ser	Ser	Ala	Arg	Met	Val	Thr	Thr	Val	
233	815					820					825					830	
235	ccc	cat	gtg	ttt	tca	aaa	ctg	tta	gaa	atg	ctg	agt	gtt	tcc	agt	tcc	2544
236	Pro	His	Val	Phe	Ser	Lys	Leu	Leu	Glu	Met	Leu	Ser	Val	Ser	Ser	Ser	
237				835						840					845		
239	act	cac	ttc	acc	agg	atg	cgt	cgc	cgt	ttg	atg	gct	att	gca	gat	gag	2592
240	Thr	His	Phe	Thr	Arg	Met	Arg	Arg	Arg	Leu	Met	Ala	Ile	Ala	Asp	Glu	
241				850					855					860			
243	gtg	gaa	att	gcc	gaa	gcc	atc	cag	ttg	ggc	gta	gaa	gac	act	ttg	gat	2640
244	Val	Glu	Ile	Ala	Glu	Ala	Ile	Gln	Leu	Gly	Val	Glu	Asp	Thr	Leu	Asp	
245				865				870					875				
247	ggg	caa	cag	gac	agc	ttc	ttg	cag	gca	tct	gtt	ccc	aac	aac	tat	ctg	2688
248	Gly	Gln	Gln	Asp	Ser	Phe	Leu	Gln	Ala	Ser	Val	Pro	Asn	Asn	Tyr	Leu	
249				880			885					890					
251	gaa	acc	aca	gag	aac	agt	tcc	cct	gag	tgc	aca	gtc	cat	tta	gag	aaa	2736
252	Glu	Thr	Thr	Glu	Asn	Ser	Ser	Pro	Glu	Cys	Thr	Val	His	Leu	Glu	Lys	
253	895					900					905					910	
255	act	gga	aaa	gga	tta	tgt	gct	aca	aaa	ttg	agt	gcc	agt	tca	gag	gac	2784
256	Thr	Gly	Lys	Gly	Leu	Cys	Ala	Thr	Lys	Leu	Ser	Ala	Ser	Ser	Glu	Asp	
257				915						920					925		
259	att	tct	gag	aga	ctg	gcc	agc	att	tca	gta	gga	cct	tct	agt	tca	aca	2832
260	Ile	Ser	Glu	Arg	Leu	Ala	Ser	Ile	Ser	Val	Gly	Pro	Ser	Ser	Ser	Thr	
261				930					935					940			
263	aca	aca	aca	aca	aca	aca	aca	gag	caa	cca	aag	cca	atg	gtt	caa	aca	2880

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264	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Glu	Gln	Pro	Lys	Pro	Met	Val	Gln	Thr	
265			945					950					955				
267	aaa	ggc	aga	ccc	cac	agc	cag	tgt	ttg	aac	tcc	tct	cct	tta	tct	cat	2928
268	Lys	Gly	Arg	Pro	His	Ser	Gln	Cys	Leu	Asn	Ser	Ser	Pro	Leu	Ser	His	
269		960					965				970						
271	cat	tcc	caa	tta	atg	ttt	cca	gcc	ttg	tca	acc	cct	tct	tct	tct	acc	2976
272	His	Ser	Gln	Leu	Met	Phe	Pro	Ala	Leu	Ser	Thr	Pro	Ser	Ser	Ser	Thr	
273	975					980				985					990		
275	cca	tct	gta	cca	gct	ggc	act	gca	aca	gat	gtc	tct	aag	cat	aga	ctt	3024
276	Pro	Ser	Val	Pro	Ala	Gly	Thr	Ala	Thr	Asp	Val	Ser	Lys	His	Arg	Leu	
277				995					1000						1005		
279	cag	gga	ttc	att	ccc	tgc	aga	ata	cct	tct	gca	tct	cct	caa	aca		3069
280	Gln	Gly	Phe	Ile	Pro	Cys	Arg	Ile	Pro	Ser	Ala	Ser	Pro	Gln	Thr		
281			1010						1015					1020			
283	cag	cgc	aag	ttt	tct	cta	caa	ttc	cac	aga	aac	tgt	cct	gaa	aac		3114
284	Gln	Arg	Lys	Phe	Ser	Leu	Gln	Phe	His	Arg	Asn	Cys	Pro	Glu	Asn		
285			1025						1030					1035			
287	aaa	gac	tca	gat	aaa	ctt	tcc	cca	gtc	ttt	act	cag	tca	aga	ccc		3159
288	Lys	Asp	Ser	Asp	Lys	Leu	Ser	Pro	Val	Phe	Thr	Gln	Ser	Arg	Pro		
289			1040						1045					1050			
291	ttg	ccc	tcc	agt	aac	ata	cac	agg	cca	aag	cca	tct	aga	cct	acc		3204
292	Leu	Pro	Ser	Ser	Asn	Ile	His	Arg	Pro	Lys	Pro	Ser	Arg	Pro	Thr		
293			1055						1060					1065			
295	cca	ggt	aat	aca	agt	aaa	cag	gga	gat	ccc	tca	aaa	aat	agc	atg		3249
296	Pro	Gly	Asn	Thr	Ser	Lys	Gln	Gly	Asp	Pro	Ser	Lys	Asn	Ser	Met		
297			1070						1075					1080			
299	aca	ctt	gat	ctg	aac	agt	agt	tcc	aaa	tgt	gat	gac	agc	ttt	ggc		3294
300	Thr	Leu	Asp	Leu	Asn	Ser	Ser	Ser	Lys	Cys	Asp	Asp	Ser	Phe	Gly		
301			1085						1090					1095			
303	tgt	agc	agc	aat	agt	agt	aat	gct	gtt	ata	ccc	agt	gac	gag	aca		3339
304	Cys	Ser	Ser	Asn	Ser	Ser	Asn	Ala	Val	Ile	Pro	Ser	Asp	Glu	Thr		
305			1100						1105					1110			
307	gtg	ttc	acc	cca	gta	gag	gag	aaa	tgc	aga	tta	gat	gtc	aat	aca		3384
308	Val	Phe	Thr	Pro	Val	Glu	Glu	Lys	Cys	Arg	Leu	Asp	Val	Asn	Thr		
309			1115						1120					1125			
311	gag	ctc	aac	tcc	agt	att	gag	gac	ctt	ctt	gaa	gca	tct	atg	cct		3429
312	Glu	Leu	Asn	Ser	Ser	Ile	Glu	Asp	Leu	Leu	Glu	Ala	Ser	Met	Pro		
313			1130						1135					1140			
315	tca	agt	gat	aca	aca	gta	act	ttt	aag	tca	gaa	gtt	gct	gtc	ctg		3474
316	Ser	Ser	Asp	Thr	Thr	Val	Thr	Phe	Lys	Ser	Glu	Val	Ala	Val	Leu		
317			1145						1150					1155			
319	tct	cct	gaa	aag	gct	gaa	aat	gat	gat	acc	tac	aaa	gat	gat	gtg		3519
320	Ser	Pro	Glu	Lys	Ala	Glu	Asn	Asp	Asp	Thr	Tyr	Lys	Asp	Asp	Val		
321			1160						1165					1170			
323	aat	cat	aat	caa	aag	tgc	aaa	gag	aag	atg	gaa	gct	gaa	gaa	gaa		3564
324	Asn	His	Asn	Gln	Lys	Cys	Lys	Glu	Lys	Met	Glu	Ala	Glu	Glu	Glu		
325			1175						1180					1185			
327	gaa	gct	tta	gca	att	gcc	atg	gca	atg	tca	gcg	tct	cag	gat	gcc		3609
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